

Please replace paragraphs 0039, 0040 and 0041 with the following rewritten paragraphs, respectively:

Figure 13 (SEQ ID NOS 34-42, respectively, in order of appearance) illustrates a first peptide sequence pileup of HAL from various bacteria, including *Corynebacteriaceae*, *B. subtilis*, *S. griseus*, *P. putida*.

A2 **Figure 14** (SEQ ID NOS 43-64, respectively, in order of appearance) is a second peptide sequence pileup of HAL from various bacteria, including *Corynebacteriaceae*, *S. griseus*, and *D. radiodurans*

Figure 15 (SEQ ID NOS 65-66, respectively, in order of appearance) is a comparison between the amino acid sequence of *S. griseus* ("STRG") and *Corynebacteriaceae* ("HAL"); positions of an amino acid identity are delineated by "**".

Please replace paragraph 00127 with the following rewritten paragraph:

Sub B2
A3 Two of the resulting probes (TM63 and TM74), shown in Table 1, below, were labeled, mixed, and used to screen the above genomic library. Oligos were labeled with $\gamma^{32}\text{P}$ ATP using T4 polynucleotide kinase as described (Ausubel, *et al*, eds, 1994. "Current Protocols in Molecular Biology," John Wiley and Sons, Inc.,) and cleaned up using Elutipis (Schleicher & Schuell). Hybridization of duplicate filters was carried out in a Bellco hybridization oven at 37°C using the SSPE protocol as described (Ausubel, *et al*, eds, "Current Protocols in Molecular Biology," John Wiley and Sons, Inc., 1994). Filters were washed in 6X SSC with 0.5%SDS (Ausubel, *et al*, eds, "Current Protocols in Molecular Biology," John Wiley and Sons, Inc., 1994) at 37°C. Filters were then washed at successively higher temperatures in 3 M TMAC (Ausubel, *et al*, eds, "Current Protocols in Molecular Biology," John Wiley and Sons, Inc., 1994) until very little radioactivity could be detected with a survey meter (generally 45 - 55°C). Upon exposure to X-Ray film (Kodak X-Omat), colonies which were evident on both replicate filters were picked with a wooden toothpick and

transferred to a fresh nylon filter overlaid onto an LB/ampicillin plate. This procedure was repeated until a homogeneous population was achieved.

Table 1: oligonucleotides (SEQ ID NOS 1-27, respectively, in order of appearance) with DNA sequence and approximate coordinates relative to the ATG start codon.

Name	Length	Sequence (5' to 3')	Coordinates
TM63	30	CGCGTTCAGGACGCATACTCCGTTTCGCTGC	838-867
TM74	24	GCCCATGGAAACGTGGTCTTCCTG	1370 - 1393
TM85	21	ATCATCATGCCCCGAGTCCACA	1156 - 1176
TM87	21	GCCATCAGGAAGACCACGTTT	990 - 971
TM89	20	ATGCAGGAAGACCACGTTTC	1246 - 1265
TM91	21	ATCGAGGTCCGCCAATGCCAT	648 - 628
TM92	18	ACCGGAGCAGGCCAGTGA	441 - 424
TM93	20	TGCTTGAAGTATTGCGCCAG	1403 - 1422
TM94	18	GATCCTCGGGTGCGATGT	226 - 209
TM95	18	ATGCTGATCGGGCTTCGT	92 - 74
TM96	27	ATTTGATT <u>CATATGGCT</u> TCCGCTCCTC	-11 - +16
TM97	28	ATCTTGGATCCGAACATGGTGCGTTGCA	Beyond C-Terminus
TM98	18	AGCACCAGAT CGATGCAC	128 - 145
TM99	18	TGGCATGGGTGAACCGGT	267 - 284
TM101	18	ATCAGCGTTGAAGCCCAG	682 - 699
TM103	18	ACGTGCTGGACTTCCTTG	1019 - 1036
TM105	18	GTGCATAAGGCCCTCGAA	1501 - 1518